

**Amendments to the Specification:**

Please replace paragraph [0080], with the following rewritten paragraph:

Software packages and databases for determining, e.g., antigenic fragments, leader sequences, protein folding, functional domains, glycosylation sites, and sequence alignments, are available (see, e.g., GenBank, Vector NTI<sup>®</sup> Suite sequence analysis and data management software (Informax, Inc, Bethesda, MD); GCG Wisconsin Package (Accelrys, Inc., San Diego, CA); DeCypher<sup>®</sup> software package (TimeLogic Corp., Crystal Bay, Nevada); Menne, *et al.* (2000) *Bioinformatics* 16: 741-742; Menne, *et al.* (2000) *Bioinformatics Applications Note* 16:741-742; Wren, *et al.* (2002) *Comput. Methods Programs Biomed.* 68:177-181; von Heijne (1983) *Eur. J. Biochem.* 133:17-21; von Heijne (1986) *Nucleic Acids Res.* 14:4683-4690).

Please replace the heading for Table 1 at page 26 with the following rewritten heading:

Table 1. Expression of subunits of p19 and IL-23R by Taqman<sup>®</sup> real time quantitative PCR analysis, relative to ubiquitin (1.0). The values are from diseased and adjacent normal tissues, where indicated.

Please replace the title on the Abstract at page 36 with the following corrected title:

~~USES OF MAMMALIAN CYTOKINE MOLECULE; RELATED REAGENTS~~ USES OF IL-23 AGONISTS AND ANTAGONISTS; RELATED REAGENTS.